

PATENT

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5-16-02

GNE.2630P1C11



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ashkenazi et al.) Group Art Unit Unknown
App. No. : 09/978,295)
Filed : October 15, 2001)
For : SECRETED AND)
TRANSMEMBRANE)
POLYPEPTIDES AND)
NUCLEIC ACIDS ENCODING)
THE SAME)
Examiner : Unknown)

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SUPPLEMENTAL INFORMATION DISCLOSURE STATEMENT

United States Patent and Trademark Office
PO Box 2327
Arlington, VA 22202


Dear Sir:

Enclosed is form PTO-1449 listing 2 references that are also enclosed. This Information Disclosure Statement is being filed before the receipt of a first Office Action on the merits, and presumably no fee is required in accordance with 37 C.F.R. § 1.97(b)(3). If a first Office Action on the merits was mailed before the mailing date of this Statement, the Commissioner is authorized to charge the fee set forth in 37 C.F.R. § 1.17(p) to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: April 30, 2002

By: 
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FORM PTO-1449

U.S. DEPARTMENT OF COMMERCE
PATENT AND TRADEMARK OFFICEATTY. DOCKET NO.
GNE.2630P1C11APPLICATION NO.
09/978,295INFORMATION DISCLOSURE STATEMENT
BY APPLICANT

(USE SEVERAL SHEETS IF NECESSARY)

APPLICANT
Ashkenazi et al.FILING DATE
October 15, 2001GROUP
Unknown

EXAMINER INITIAL	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)
	1. Blast Results A1-A10 (Alignment of DNA40571 and various nucleotide sequences - GenBank Database), October 4, 2001
	2. Blast Results B1-B2 (Alignment of DNA40571 and various polypeptide sequences - Dayhoff Database), October 3, 2001

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Thu Oct 4 09:05:04 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpenda/temp4/ss.DNA40571 (2365 bp)

Sequences producing High-scoring Segment Pairs:	Frame	Score	Match	Pct	E-val
1 P_AAA37664 Human peptidase, HPEP-8 coding sequence.	+	1334	1340	100	0.0
2 P_AAF30189 Clone 11618130.0.27 encoding secreted pr	+	1321	1345	99	0.0
3 AX079872 Sequence 3 from Patent WO0105971.	+	1321	1345	99	0.0
4 P_AAF30195 Clone 11618130.0.184 encoding secreted p	+	762	765	100	0.0
5 AX079884 Sequence 15 from Patent WO0105971.	+	762	765	100	0.0

>1 P_AAA37664 Human peptidase, HPEP-8 coding sequence. DNA, PAT 24-OCT-2000
(1661 bp) [2 segs]
Score = 1334 (2644 bits), Expect = 0.0 [P_AAA37664, seg 1/2]
Identities = 1340/1342 (99%), at 1010,320-2351,1661, Strand +/+

```

DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTTCAGGCT
*****
P_AAA37664 320 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTTCAGGCT

DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
*****
P_AAA37664 380 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC

DNA40571 1130 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCTGGCCAG
*****
P_AAA37664 440 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCTGGCCAG

DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
*****
P_AAA37664 500 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC
*****
P_AAA37664 560 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC
*****
P_AAA37664 620 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC

DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG
*****
P_AAA37664 680 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG

DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
*****

```

P_AAA37664 740 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC

DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC

P_AAA37664 800 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC

DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA

P_AAA37664 860 CTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA

DNA40571 1610 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG

P_AAA37664 920 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG

DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

P_AAA37664 980 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

DNA40571 1730 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCA

P_AAA37664 1040 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCA

DNA40571 1790 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGGCTGCACAGCTTCGGAGAT

P_AAA37664 1100 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGGCTGCACAGCTTCGGAGAT

DNA40571 1850 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG

P_AAA37664 1160 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG

DNA40571 1910 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCCGAGGCTGAGCCT

P_AAA37664 1220 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCCGAGGCTGAGCCT

DNA40571 1970 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC

P_AAA37664 1280 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC

DNA40571 2030 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGT

P_AAA37664 1340 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGT

DNA40571 2090 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT

P_AAA37664 1400 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT

DNA40571 2150 GCCTGGGGCCACAGGTGCCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC

P_AAA37664 1460 GCCTGGGGCCACAGGTGCCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC

DNA40571 2210 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTCAGA

P_AAA37664 1520 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGA

DNA40571 2270 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTGGGGGCAGCAGTTTCC

P_AAA37664 1580 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTGGGGGCAGCAGTTTCC

DNA40571 2330 TTTTTTTAACTTAAATAAATT

 P_AAA37664 1640 TTTTTTTAACTTAAATAAATT

Score = 170 (337 bits), Expect = 8e-89 [P_AAA37664, seg 2/2]
 Identities = 170/170 (100%), at 844,1-1013,170, Strand +/+

DNA40571 844 GGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCC

 P_AAA37664 1 GGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCC

 DNA40571 904 CACATGTAAGTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCC

 P_AAA37664 61 CACATGTAAGTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCC

 DNA40571 964 TGGGATGCTATGTGGGGGCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

 P_AAA37664 121 TGGGATGCTATGTGGGGGCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

>2 P_AAF30189 Clone 11618130.0.27 encoding secreted protein SECP2. (1894 bp) [3
 segs]

Score = 1321 (2619 bits), Expect = 0.0 [P_AAF30189, seg 1/3]
 Identities = 1345/1353 (99%), at 1010,534-2362,1886, Strand +/+

DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT

 P_AAF30189 534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT

 DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC

 P_AAF30189 594 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC

 DNA40571 1130 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG

 P_AAF30189 654 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG

 DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

 P_AAF30189 714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

 DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

 P_AAF30189 774 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

 DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC

 P_AAF30189 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC

 DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG

 P_AAF30189 894 CACTGCTTCAATGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG

 DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC

 P_AAF30189 954 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC

DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC

P_AAF30189 1014 TACGACATGGCCCTCCTGCTGCTGGCTCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCC

DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA

P_AAF30189 1074 CTCTGCCTGCCCTATTTTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTCTCTGGGA

DNA40571 1610 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG

P_AAF30189 1134 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG

DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

P_AAF30189 1194 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

DNA40571 1730 GGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA

P_AAF30189 1254 GGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA

DNA40571 1790 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGAT

P_AAF30189 1314 CCACTGGTGCATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGAT

DNA40571 1850 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG

P_AAF30189 1374 GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG

DNA40571 1910 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT

P_AAF30189 1434 GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT

DNA40571 1970 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC

P_AAF30189 1494 GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC

DNA40571 2030 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCTCCCCACCCTGT

P_AAF30189 1554 TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCTCCCCACCCTGT

DNA40571 2090 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT

P_AAF30189 1614 CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT

DNA40571 2150 GCCTGGGGCCACAGGTGCCCCCTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC

P_AAF30189 1674 GCCTGGGGCCACAGGTGCCCCCTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC

DNA40571 2210 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTTCTCAGA

P_AAF30189 1734 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTTCTCAGA

DNA40571 2270 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCC

P_AAF30189 1794 TACAATCACGCCAGCCCCGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCC

DNA40571 2330 TTTTTTTAACTTAAATAAATTGTTACAAAATA

P_AAF30189 1854 TTTTAACTTAAATAAATTGTTACAAAATA

Score = 157 (311 bits), Expect = 5e-81 [P_AAF30189, seg 2/3]
Identities = 157/157 (100%), at 857,228-1013,384, Strand +/+

```
DNA40571 857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT
*****
P_AAF30189 228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT

DNA40571 917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT
*****
P_AAF30189 288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT

DNA40571 977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCCTGTCAGG
*****
P_AAF30189 348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCCTGTCAGG
```

Score = 87 (172 bits), Expect = 3e-39 [P_AAF30189, seg 3/3]
Identities = 87/87 (100%), at 771,1-857,87, Strand +/+

```
DNA40571 771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA
*****
P_AAF30189 1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA

DNA40571 831 CTGGCTGGGATCAGGACACCAGTGATG
*****
P_AAF30189 61 CTGGCTGGGATCAGGACACCAGTGATG
```

>3 AX079872 Sequence 3 from Patent WO0105971. (1894 bp) [3 segs]
Score = 1321 (2619 bits), Expect = 0.0 [AX079872, seg 1/3]
Identities = 1345/1353 (99%), at 1010,534-2362,1886, Strand +/+

```
DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT
*****
AX079872 534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT

DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
*****
AX079872 594 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC

DNA40571 1130 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG
*****
AX079872 654 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG

DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
*****
AX079872 714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC
*****
AX079872 774 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTGCTGCC
*****
AX079872 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTGCTGCC
```

DNA40571	1370	CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG *****
AX079872	894	CACTGCTTCAATGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG
DNA40571	1430	GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG *****
AX079872	954	GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
DNA40571	1490	TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCC ***** **
AX079872	1014	TACGACATGGCCCTCCTGCTGCTGGCTCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCC
DNA40571	1550	CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA *****
AX079872	1074	CTCTGCCTGCCCTATTTTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA
DNA40571	1610	CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCCTGGGG *****
AX079872	1134	CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCCTGGGG
DNA40571	1670	CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG *****
AX079872	1194	CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG
DNA40571	1730	GGGATGGTGTGTACCAGTGTCTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA *****
AX079872	1254	GGGATGGTGTGTACCAGTGTCTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA
DNA40571	1790	CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGCTGCACAGCTTCGGAGAT *****
AX079872	1314	CCACTGGTGCATGAGGTGAGGGGCACATGGTTCTTGCCGGGCTGCACAGCTTCGGAGAT
DNA40571	1850	GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG *****
AX079872	1374	GCTTGCCAAGGCCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGG
DNA40571	1910	GTCAGCAGTTTGGAAGTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT *****
AX079872	1434	GTCAGCAGTTTGGAAGTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCT
DNA40571	1970	GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC *****
AX079872	1494	GGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTC
DNA40571	2030	TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGT *****
AX079872	1554	TCAGGACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCTGT
DNA40571	2090	CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT *****
AX079872	1614	CATGTGTGATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCT
DNA40571	2150	GCCTGGGGCCACAGGTGCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC *****
AX079872	1674	GCCTGGGGCCACAGGTGCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCC
DNA40571	2210	CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCTTTACTCTTTCAGA


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*****
AX079872  1734 CACACCCAACCTCTGCTACCAAGCAGGCGTCTCAGCTTTCCTCCTCTTTACCCTTTTCAGA
DNA40571  2270 TACAATCACGCCAGCCACGTTGTTTTGAAAATTTCTTTTTTTTGGGGGGCAGCAGTTTTCC
*****
AX079872  1794 TACAATCACGCCAGCCCCGTTGTTTTGAAAATTTCTTTTTTTTGGGGGGCAGCAGTTTTCC
DNA40571  2330 TTTTTTTAACTTAAATAAATTGTTACAAAATA
*****
AX079872  1854 TTTTTTTAACTTAAATAAATTGTTACAAAATA

```

Score = 157 (311 bits), Expect = 5e-81 [AX079872, seg 2/3]
Identities = 157/157 (100%), at 857,228-1013,384, Strand +/-

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DNA40571  857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT
*****
AX079872  228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT
DNA40571  917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT
*****
AX079872  288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT
DNA40571  977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG
*****
AX079872  348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

```

Score = 87 (172 bits), Expect = 3e-39 [AX079872, seg 3/3]
Identities = 87/87 (100%), at 771,1-857,87, Strand +/-

```

DNA40571  771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA
*****
AX079872   1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA
DNA40571  831 CTGGCTGGGATCAGGACACCAAGTGATG
*****
AX079872   61 CTGGCTGGGATCAGGACACCAAGTGATG

```

>4 P_AAF30195 Clone 11618130.0.184 encoding secreted protein SECP8. (1445 bp) [3
segs]

Score = 762 (1511 bits), Expect = 0.0 [P_AAF30195, seg 1/3]
Identities = 765/766 (99%), at 1010,534-1775,1299, Strand +/-

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DNA40571  1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT
*****
P_AAF30195  534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT
DNA40571  1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
*****
P_AAF30195  594 GGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
DNA40571  1130 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCCAG
*****
P_AAF30195  654 ACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCCAG
DNA40571  1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
*****
P_AAF30195  714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

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DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

 P_AAF30195 774 ACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC
 DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC

 P_AAF30195 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC
 DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG

 P_AAF30195 894 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG
 DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC

 P_AAF30195 954 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC
 DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC

 P_AAF30195 1014 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC
 DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA

 P_AAF30195 1074 CTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGA
 DNA40571 1610 CGGGCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG

 P_AAF30195 1134 CGGGCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGG
 DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

 P_AAF30195 1194 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG
 DNA40571 1730 GGGATGGTGTGTACCAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG

 P_AAF30195 1254 GGGATGGTGTGTACCAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG

Score = 157 (311 bits), Expect = 5e-81 [P_AAF30195, seg 2/3]
 Identities = 157/157 (100%), at 857,228-1013,384, Strand +/+

DNA40571 857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGT

 P_AAF30195 228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGT
 DNA40571 917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGCCTGGGATGCTATGT

 P_AAF30195 288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGCCTGGGATGCTATGT
 DNA40571 977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCTGTCAGG

 P_AAF30195 348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCTGTCAGG

Score = 87 (172 bits), Expect = 3e-39 [P_AAF30195, seg 3/3]
 Identities = 87/87 (100%), at 771,1-857,87, Strand +/+

DNA40571 771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA

P_AAF30195 1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA
DNA40571 831 CTGGCTGGGATCAGGACACCAGTGATG

P_AAF30195 61 CTGGCTGGGATCAGGACACCAGTGATG

>5 AX079884 Sequence 15 from Patent W00105971. (1445 bp) [3 segs]
Score = 762 (1511 bits), Expect = 0.0 [AX079884, seg 1/3]
Identities = 765/766 (99%), at 1010,534-1775,1299, Strand +/-

DNA40571 1010 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT

AX079884 534 CAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCT
DNA40571 1070 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC

AX079884 594 GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC
DNA40571 1130 ACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG

AX079884 654 ACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAG
DNA40571 1190 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG

AX079884 714 AGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
DNA40571 1250 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC

AX079884 774 ACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCAC
DNA40571 1310 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC

AX079884 834 CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTGCTGCC
DNA40571 1370 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG

AX079884 894 CACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCG
DNA40571 1430 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC

AX079884 954 GAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGC
DNA40571 1490 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC

AX079884 1014 TACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCC
DNA40571 1550 CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCCTGGGA

AX079884 1074 CTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCCTGGGA
DNA40571 1610 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGGCCGTGACCCTCCTGGGG

AX079884 1134 CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGGCCGTGACCCTCCTGGGG
DNA40571 1670 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

AX079884 1194 CCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG

DNA40571 1730 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG

AX079884 1254 GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGG

Score = 157 (311 bits), Expect = 5e-81 [AX079884, seg 2/3]
Identities = 157/157 (100%), at 857,228-1013,384, Strand +/+

DNA40571 857 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT

AX079884 228 GCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGT

DNA40571 917 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT

AX079884 288 ATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGT

DNA40571 977 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

AX079884 348 GGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGG

Score = 87 (172 bits), Expect = 3e-39 [AX079884, seg 3/3]
Identities = 87/87 (100%), at 771,1-857,87, Strand +/+

DNA40571 771 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA

AX079884 1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCA

DNA40571 831 CTGGCTGGGATCAGGACACCAAGTGATG

AX079884 61 CTGGCTGGGATCAGGACACCAAGTGATG

Wed Oct 3 10:32:47 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]
/home/ruby/va/Molbio/carpenda/new.pro/pl.DNA40571.nc (347 aa)

Sequences producing High-scoring Segment Pairs:				Score	Match	Pct	E-val
1	P_AAB24046	Human PRO351 protein sequence	SEQ ID NO:1	1897	347	100	0.0
2	P_AAB44260	Human PRO351 (UNQ308) protein sequence	SE	1897	347	100	0.0
3	P_AAY41704	Human PRO351 protein sequence	- Homo sapi	1897	347	100	0.0

>1 P_AAB24046 Human PRO351 protein sequence SEQ ID NO:12 - Homo sapiens. (571 aa) [2 segs]

Score = 1897 (735 bits), Expect = 0.0 [P_AAB24046, seg 1/2]
Identities = 347/347 (100%), Positives = 347/347 (100%), at 1,225-347,571

DNA40571.nc	1	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS

P_AAB24046	225	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
DNA40571.nc	61	WLQARVQGAAFLAQSPETPEMSDEDSVCACGSLRTAGPQAGAPSPWPWEARLMHQQLAC

P_AAB24046	285	WLQARVQGAAFLAQSPETPEMSDEDSVCACGSLRTAGPQAGAPSPWPWEARLMHQQLAC
DNA40571.nc	121	GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL

P_AAB24046	345	GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
DNA40571.nc	181	LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPTLLGPRACSR

P_AAB24046	405	LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPTLLGPRACSR
DNA40571.nc	241	LHAAPGGDGSPIPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSGFDACQGPA

P_AAB24046	465	LHAAPGGDGSPIPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSGFDACQGPA
DNA40571.nc	301	RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC

P_AAB24046	525	RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC

>2 P_AAB44260 Human PRO351 (UNQ308) protein sequence SEQ ID NO:132 - Homo (571 aa) [2 segs]

Score = 1897 (735 bits), Expect = 0.0 [P_AAB44260, seg 1/2]
Identities = 347/347 (100%), Positives = 347/347 (100%), at 1,225-347,571

DNA40571.nc	1	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS

P_AAB44260	225	MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
DNA40571.nc	61	WLQARVQGAAFLAQSPETPEMSDEDSVCACGSLRTAGPQAGAPSPWPWEARLMHQQLAC

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P_AAB44260 285 WLQARVQGAAFLAQSPETPEMSDEDSVCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC
DNA40571.nc 121 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
*****
P_AAB44260 345 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
DNA40571.nc 181 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
*****
P_AAB44260 405 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
DNA40571.nc 241 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
*****
P_AAB44260 465 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
DNA40571.nc 301 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC
*****
P_AAB44260 525 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC
```

>3 P_AAY41704 Human PRO351 protein sequence - Homo sapiens. (571 aa) [2 segs]
Score = 1897 (735 bits), Expect = 0.0 [P_AAY41704, seg 1/2]
Identities = 347/347 (100%), Positives = 347/347 (100%), at 1,225-347,571

```
DNA40571.nc 1 MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
*****
P_AAY41704 225 MLCGGPQPGVQGPCQGDSSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS
DNA40571.nc 61 WLQARVQGAAFLAQSPETPEMSDEDSVCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC
*****
P_AAY41704 285 WLQARVQGAAFLAQSPETPEMSDEDSVCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC
DNA40571.nc 121 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
*****
P_AAY41704 345 GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL
DNA40571.nc 181 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
*****
P_AAY41704 405 LLAQPVTLGASLRPLCLPYPDHHLDPDGERGWVLGRARPGAGISSLQTVPVTLTGPRACSR
DNA40571.nc 241 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
*****
P_AAY41704 465 LHAAPGGDGSPIPLPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPA
DNA40571.nc 301 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC
*****
P_AAY41704 525 RPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC
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